0400

0207

OIPE

RAW SEQUENCE LISTING DATE: 03/01/2001
PATENT APPLICATION: US/09/775,009 TIME: 09:37:54

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\02282001\I775009.raw

ENTERED

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  3 <110> APPLICANT: Chiang, Lillian Wei-Ming
  5 <120> TITLE OF INVENTION: NARC8 Programmed Cell Death-Associated
  6       Molecule and Uses Thereof
 10 <130> FILE REFERENCE: 35800/207197
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/775,009
C--> 12 <141> CURRENT FILING DATE: 2001-02-01
 12 <150> PRIOR APPLICATION NUMBER: 09/692,785
 13 <151> PRIOR FILING DATE: 2000-10-20
 15 <150> PRIOR APPLICATION NUMBER: 60/161,188
 16 <151> PRIOR FILING DATE: 1999-10-22
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 34 tccgccgagc ctgcccgggt ccgggcgctt gtctatgggc accacgggga tccagccaag    180
 35 gtcgtcgaaa ccgtaattcc tgggcacaca tggcagctca gaaatgttgc ctgacctact    240
 36 ttgaggagat gatttgagcg aaacacccat tctagcctgg atgacatgaa catctccgtt    300
 37 tggctttgtg cttagactca agaacctgga gctagctgct gtgagaggat cagatgtccg    360
 38 tgtgaag atg ctg gcg gcc cct atc aat cca tct gac ata aat atg atc      409
 39         Met Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile
 40          1               5                  10
 42 caa gga aac tac gga ctc ctt cct gaa ctg cct gct gtt gga ggg aac      457
 43 Gln Gly Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn
 44  15                  20                  25                  30
 46 gaa ggt gtt gca cag gtg gta gcg gtg ggc agc aat gtg acc ggg ctg      505
 47 Glu Gly Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu
 48                  35                  40                  45
 50 aag cca gga gac tgg gtg att cca gca aat gct ggt tta gga acc tgg      553
 51 Lys Pro Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp
 52              50                  55                  60
 54 cgg acc gag gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt      601
 55 Arg Thr Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser
 56          65                  70                  75
 58 gac atc cct ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca      649
 59 Asp Ile Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr
 60      80                  85                  90
 62 gcc tac agg atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct      697
 63 Ala Tyr Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser
 64  95                  100                 105                 110
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66 gtc atc cag aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag      745
67 Val Ile Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln
68                 115                 120                 125
70 atc gcc gca gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga      793
71 Ile Ala Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg
72             130                 135                 140
74 cct gat atc cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag      841
75 Pro Asp Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu
76         145                 150                 155
78 cat gtc atc aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc      889
79 His Val Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe
80     160                 165                 170
82 ttt aag gac atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg      937
83 Phe Lys Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly
84 175                 180                 185                 190
86 aaa agc tcc aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg      985
87 Lys Ser Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met
88                 195                 200                 205
90 gta acc tat ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc     1033
91 Val Thr Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser
92             210                 215                 220
94 ctg ctc att ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag     1081
95 Leu Leu Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln
96         225                 230                 235
98 tgg aag aag gat cac agt cca gac cag ttc aag gag ctg atc ctc aca     1129
99 Trp Lys Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr
100     240                 245                 250
102 ctg tgc gat ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc     1177
103 Leu Cys Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser
104 255                 260                 265                 270
106 cag gtc ccg ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag     1225
107 Gln Val Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys
108                 275                 280                 285
110 ccc ttc ata tct tca aag cag att ctc acc atg tga tcatcccaaa          1271
111 Pro Phe Ile Ser Ser Lys Gln Ile Leu Thr Met  *
112             290                 295
114 agagctggag tgacatggga ggggaggcgg atctgagggg ctgggtgcag gcccctcagt   1331
115 tggggctccc accttcccca gactactgtt ctcctcactg cctcttccta ttaggaggat   1391
116 ggtgaagcca gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac   1451
117 tctcccttcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa       1507
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 297
121 <212> TYPE: PRT
122 <213> ORGANISM: Homo sapiens
124 <400> SEQUENCE: 2
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127 Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly
128             20                  25                  30
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129 Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro
130         35                  40                  45
131 Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr
132     50                  55                  60
133 Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile
134 65                  70                  75                  80
135 Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr
136                 85                  90                  95
137 Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile
138             100                 105                 110
139 Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala
140         115                 120                 125
141 Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp
142     130                 135                 140
143 Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val
144 145                 150                 155                 160
145 Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys
146                 165                 170                 175
147 Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser
148             180                 185                 190
149 Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr
150         195                 200                 205
151 Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu
152     210                 215                 220
153 Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys
154 225                 230                 235                 240
155 Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys
156                 245                 250                 255
157 Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val
158             260                 265                 270
159 Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe
160         275                 280                 285
161 Ile Ser Ser Lys Gln Ile Leu Thr Met
162     290                 295
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165 <211> LENGTH: 894
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapiens
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171 cttcctgaac tgcctgctgt tggagggaac gaaggtgttg cacaggtggt agcggtgggc     120
172 agcaatgtga ccgggctgaa gccaggagac tgggtgattc cagcaaatgc tggtttagga     180
173 acctggcgga ccgaggctgt gttcagcgag gaagcactga tccaagttcc gagtgacatc     240
174 cctcttcaga gcgctgccac cctgggtgtc aatccctgca cagcctacag gatgttgatg     300
175 gatttcgagc aactgcagcc aggggattct gtcatccaga atgcatccaa cagcggagtg     360
176 gggcaagcgg tcatccagat cgccgcagcc ctgggcctaa gaaccatcaa tgtggtccga     420
177 gacagacctg atatccagaa gctgagtgac agactgaaga gtctgggggc tgagcatgtc     480
178 atcacagaag aggagctaag aaggcccgaa atgaaaaact tctttaagga catgccccag     540
179 ccacggcttg ctctcaactg tgttggtggg aaaagctcca cagagctgct gcggcagtta     600
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Input Set : A:\Seqlist.txt
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aaggatcaca gtccagacca gttcaaggag ctgatcctca cactgtgcga tctcatccgc     780
cgaggccagc tcacagcccc tgcctgctcc caggtcccgc tgcaggacta ccagtctgcc     840
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gcc cgg cag tgg cgg ggg ctg ctc cca gct tct ggc tgt cac gga cct       99
Ala Arg Gln Trp Arg Gly Leu Leu Pro Ala Ser Gly Cys His Gly Pro
      15                  20                  25
gcc gcc tcc tcc tac tcc gca tcc gcc gag cct gcc cgg gtc cgg gcg      147
Ala Ala Ser Ser Tyr Ser Ala Ser Ala Glu Pro Ala Arg Val Arg Ala
 30                  35                  40                  45
ctt gtc tat ggg cac cac ggg gat cca gcc aag gtc gtc gaa ctc aag      195
Leu Val Tyr Gly His His Gly Asp Pro Ala Lys Val Val Glu Leu Lys
                    50                  55                  60
aac ctg gag cta gct gct gtg aga gga tca gat gtc cgt gtg aag atg      243
Asn Leu Glu Leu Ala Ala Val Arg Gly Ser Asp Val Arg Val Lys Met
               65                  70                  75
ctg gcg gcc cct atc aat cca tct gac ata aat atg atc caa gga aac      291
Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile Gln Gly Asn
          80                  85                  90
tac gga ctc ctt cct gaa ctg cct gct gtt gga ggg aac gaa ggt gtt      339
Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly Val
      95                 100                 105
gca cag gtg gta gcg gtg ggc agc aat gtg acc ggg ctg aag cca gga      387
Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro Gly
110                 115                 120                 125
gac tgg gtg att cca gca aat gct ggt tta gga acc tgg cgg acc gag      435
Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr Glu
                130                 135                 140
gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt gac atc cct      483
Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile Pro
            145                 150                 155
ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca gcc tac agg      531
Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr Arg
        160                 165                 170
atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct gtc atc cag      579
Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile Gln
    175                 180                 185
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Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\02282001\I775009.raw

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244 aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag atc gcc gca      627
245 Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala Ala
246 190                 195                 200                 205
248 gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga cct gat atc      675
249 Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp Ile
250                 210                 215                 220
252 cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag cat gtc atc      723
253 Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile
254             225                 230                 235
256 aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc ttt aag gac      771
257 Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp
258         240                 245                 250
260 atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg aaa agc tcc      819
261 Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser
262     255                 260                 265
264 aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg gta acc tat      867
265 Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr
266 270                 275                 280                 285
268 ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc ctg ctc att      915
269 Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile
270                 290                 295                 300
272 ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag tgg aag aag      963
273 Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys
274             305                 310                 315
276 gat cac agt cca gac cag ttc aag gag ctg atc ctc aca ctg tgc gat     1011
277 Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp
278         320                 325                 330
280 ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc cag gtc ccg     1059
281 Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro
282     335                 340                 345
284 ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag ccc ttc ata     1107
285 Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile
286 350                 355                 360                 365
288 tct tca aag cag att ctc acc atg tga tcatcccaaa agagctggag          1154
289 Ser Ser Lys Gln Ile Leu Thr Met  *
290                 370
292 tgacatggga ggggaggcgg atctgagggg ctgggtgcag gcccctcagt tggggctccc   1214
293 accttcccca gactactgtt ctcctcactg cctcttccta ttaggaggat ggtgaagcca   1274
294 gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac tctcccttcc   1334
295 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                 1380
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298 <211> LENGTH: 373
299 <212> TYPE: PRT
300 <213> ORGANISM: Homo sapiens
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306             20                  25                  30
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

Application No.: 09/775,011

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

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